

SEQUENCE LISTING

<110> West, James W.
Brandt, Cameron S.
Jaspers, Stephen R.

<120> Production of Homotrimeric Fusion
Proteins

<130> 02-17

<140> 10/684,149

<141> 2003-10-10

<150> 60/417,801

<151> 2002-10-11

<160> 23

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> C-myc tag

<400> 1

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

1 5 10

<210> 2

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Hemagglutinin A epitope tag

<400> 2

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5

<210> 3
<211> 1377
<212> DNA
<213> Human

<220>
<221> CDS
<222> (14)...(892)

<400> 3
agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg 49
Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
1 5 10

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg 97
Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
15 20 25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg 145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
30 35 40

ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc 193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
45 50 55 60

acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc 241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
65 70 75

aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc 289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
80 85 90

tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc 337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
95 100 105

agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga 385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
110 115 120

gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag 433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu

125	130	135	140
cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt 481			
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser			
145	150	155	
gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529			
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys			
160	165	170	
gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag 577			
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys			
175	180	185	
agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625			
Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser			
190	195	200	
ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg 673			
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val			
205	210	215	220
agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721			
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu			
225	230	235	
tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769			
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp			
240	245	250	
ccc act tgt get gga agg tgg ggg tgc cac acc agg acc aca gtc ctg 817			
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu			
255	260	265	
cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865			
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val			
270	275	280	
cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggagagg 912			
Pro Ala Gln Glu Gly Gly Pro Gly Ala			
285	290		
aaaggaggag ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga 972			
gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032			
gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092			
ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152			

gggagagagg cagagagaca gagagggaga gagggacaga gagatataga gcaggaggtc 1212
 ggggcactct gactccagct tccagtgca gctgtaggct gtcacacct aaccacacgt 1272
 gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gcccctctc ctggagaata 1332
 aaacctttgg cagctgcct tctcaaaaa aaaaaaaaa aaaaa 1377

<210> 4
 <211> 293
 <212> PRT
 <213> Human

<400> 4
 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu

275 280 285
Gly Gly Pro Gly Ala
290

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 5
gggcctccag gccaccagg t 21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 6
tcacattgga gccactagga a 21

<210> 7
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 7
acaggtgtcc agggaattca tataggccgg ccacatgga tgcaatgaag agaggg 56

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 8

accctcaggc atcgaacccg aaccgaacc ggatcc

36

<210> 9

<211> 118

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 9

gatcggatcc atggccgaaa ctgaccta aacagtcaa gacctacca gcgtagtcca 60

gacgtcctg caagagatcg aagataagtt tcagactatg agcgacaaa tcattgag 118

<210> 10

<211> 100

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 10

agaatgcatg acatgagctc caggatagat gaccttgaga aaaatatagc agatttaatg 60

acgcaagctg gtgtggaaga gttggaagga agtgggtcta 100

<210> 11

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

gatctagaac cacttccttc caactcttcc acaccagctt gcgtcattaa atctgctata 60

ttttctcaa ggatctctat cctggagctc atgtcatcga ttctctcaat 110

<210> 12

<211> 108

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 12

gatttggtcg ctcatagtct gaaacttata ttgcattctt tgcaggagcg tctggactac 60
gctggaagg tctgaactg ttttaggata agtttcggcc atggatcc 108

<210> 13

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 13

cacacgtacg aagatggatg caatgaagag agg 33

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 14

ggttagatct cgaacccgaa cccgaaccgg 30

<210> 15

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 15

ctagaaataa tttgtttaa cttaagaag gagatatata tatggctatg agatcctgcc 60
cc 62

<210> 16

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 16

tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgatgg tgatggtgat 60
ggcc 64

<210> 17

<211> 516

<212> DNA

<213> Artificial Sequence

<220>

<223> TACI-HSBP fragment

<400> 17

atggctatga gatcctgccc cgaagagcag tactgggata ctctgctggg tacctgcatg 60
tctgcaaaa ccatttgcaa ccatcagagc cagcgacct gtgcagcctt ctgcaggtca 120
ctcagctgcc gcaaggagca aggcaagtc tatgaccatc tctgaggga ctgcatcagc 180
tgtgcctcca tctgtggaca gcaccctaag caatgtgcat acttctgtga gaacaagctc 240
aggagcggat ccggttcggg ttcggttcg agatccatgg ccgaaactga tctaaaaca 300
gttcaagacc ttaccagcgt agtcagacg ctctgcaag agatgcaaga taagttcag 360
actatgagcg accaaatcat tgagagaatc gatgacatga gctccaggat agatgacctt 420
gagaaaaata tagcagattt aatgacgcaa gctggtgtgg aagagttgga aggaagtgg 480
tctagatccg gtggccatca ccatcaccat cactga 516

<210> 18

<211> 171

<212> PRT

<213> Artificial Sequence

<220>

<223> TACI-HSBP fragment

<400> 18

Met Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
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Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
20 25 30
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
35 40 45
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
50 55 60
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
65 70 75 80
Arg Ser Gly Ser Gly Ser Gly Ser Gly Ser Arg Ser Met Ala Glu Thr
85 90 95
Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val Gln Thr Leu Leu

85

90

95

aat ggc acc cct gta atg tac acc tat gat gaa tac acc aaa ggc tac 336
 Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
 100 105 110

ctg gat cag gct tca ggg agt gcc atc atc gat ctc aca gaa aat gac 384
 Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
 115 120 125

cag gtg tgg ctc cag ctt ccc aat gcc gag tca aat ggc cta tac tcc 432
 Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser
 130 135 140

tct gag tat gtc cac tcc tct ttc tca gga ttc cta gtg gct cca atg 480
 Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met
 145 150 155 160

<210> 20

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> NC-1 fragment

<400> 20

Met Pro Glu Gly Phe Ile Lys Ala Gly Gln Arg Pro Ser Leu Ser Gly
 1 5 10 15
 Thr Pro Leu Val Ser Ala Asn Gln Arg Val Thr Gly Met Pro Val Ser
 20 25 30
 Ala Phe Thr Val Ile Leu Ser Lys Ala Tyr Pro Ala Ile Gly Thr Pro
 35 40 45
 Ile Pro Phe Asp Lys Ile Leu Tyr Asn Arg Gln Gln His Tyr Asp Pro
 50 55 60
 Arg Thr Gly Ile Phe Thr Cys Gln Ile Pro Gly Ile Tyr Tyr Phe Ser
 65 70 75 80
 Tyr His Val His Val Lys Gly Thr His Val Trp Val Gly Leu Tyr Lys
 85 90 95
 Asn Gly Thr Pro Val Met Tyr Thr Tyr Asp Glu Tyr Thr Lys Gly Tyr
 100 105 110
 Leu Asp Gln Ala Ser Gly Ser Ala Ile Ile Asp Leu Thr Glu Asn Asp
 115 120 125
 Gln Val Trp Leu Gln Leu Pro Asn Ala Glu Ser Asn Gly Leu Tyr Ser

130	135	140	
Ser Glu Tyr Val His Ser Ser Phe Ser Gly Phe Leu Val Ala Pro Met			
145	150	155	160

<210> 21
 <211> 195
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HSBP-1 fragment

<220>
 <221> CDS
 <222> (1)...(195)

<400> 21			
atg gcc gaa act gat cct aaa aca gtt caa gac ctt acc agc gta gtc	48		
Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val			
1 5 10 15			

cag acg ctc ctg caa gag atg caa gat aag ttt cag act atg agc gac	96
Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp	
20 25 30	

caa atc att gag aga atc gat gac atg agc tcc agg ata gat gac ctt	144
Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu	
35 40 45	

gag aaa aat ata gca gat tta atg acg caa gct ggt gtg gaa gag ttg	192
Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu	
50 55 60	

gaa	195
Glu	
65	

<210> 22
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HSBP-1 fragment

<400> 22

Met Ala Glu Thr Asp Pro Lys Thr Val Gln Asp Leu Thr Ser Val Val

1 5 10 15

Gln Thr Leu Leu Gln Glu Met Gln Asp Lys Phe Gln Thr Met Ser Asp

20 25 30

Gln Ile Ile Glu Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu

35 40 45

Glu Lys Asn Ile Ala Asp Leu Met Thr Gln Ala Gly Val Glu Glu Leu

50 55 60

Glu

65

<210> 23

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> RYIRS tag

<400> 23

Arg Tyr Ile Arg Ser

1 5